



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 20, 2016 – 10:56 AM EST

PDB ID : 5BP3  
Title : Dehydratase domain (DH) of a mycocerosic acid synthase-like (MAS-like) PKS, crystal form 2  
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Deposited on : 2015-05-27  
Resolution : 1.45 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20028442  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20028442

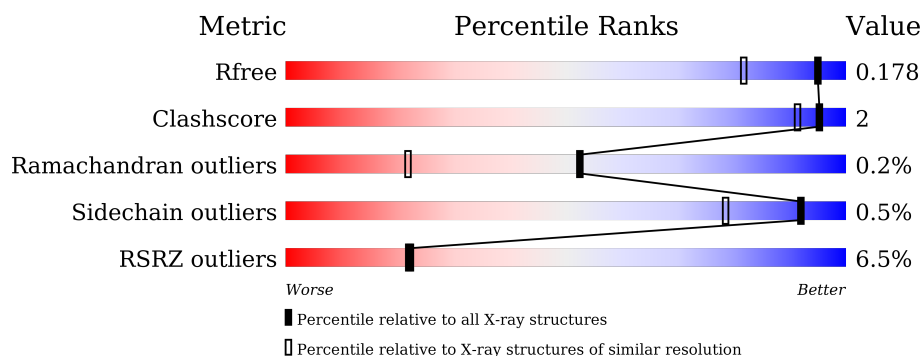
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.45 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	1278 (1.48-1.44)
Clashscore	102246	1336 (1.48-1.44)
Ramachandran outliers	100387	1320 (1.48-1.44)
Sidechain outliers	100360	1320 (1.48-1.44)
RSRZ outliers	91569	1279 (1.48-1.44)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	305	<div> <div>5%</div> <div> <div></div> <div>91%</div> <div>• 6%</div> </div> </div>
1	B	305	<div> <div>7%</div> <div> <div></div> <div>89%</div> <div>• 8%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EDO	B	1203	-	-	-	X

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9282 atoms, of which 4314 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Mycocerosic acid synthase-like polyketide synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	286	Total	C	H	N	O	S	0	28	0
			4391	1401	2157	397	427	9			
1	B	282	Total	C	H	N	O	S	0	25	0
			4334	1390	2121	402	413	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	882	SER	-	expression tag	UNP A0R1E8
A	883	MET	-	expression tag	UNP A0R1E8
B	882	SER	-	expression tag	UNP A0R1E8
B	883	MET	-	expression tag	UNP A0R1E8

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C H O 10 2 6 2	0	0
2	A	1	Total C H O 10 2 6 2	0	0
2	A	1	Total C H O 10 2 6 2	0	0
2	B	1	Total C H O 10 2 6 2	0	0
2	B	1	Total C H O 10 2 6 2	0	0
2	B	1	Total C H O 10 2 6 2	0	0

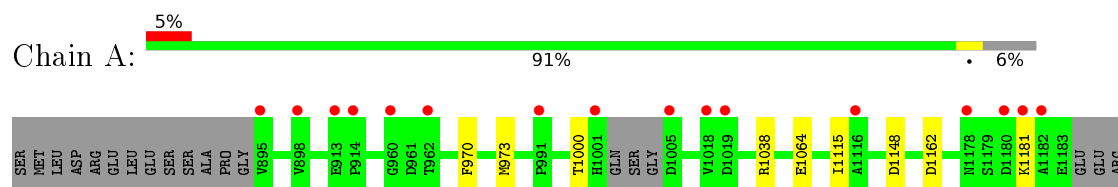
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	288	Total O 288 288	0	0
3	B	209	Total O 209 209	0	0

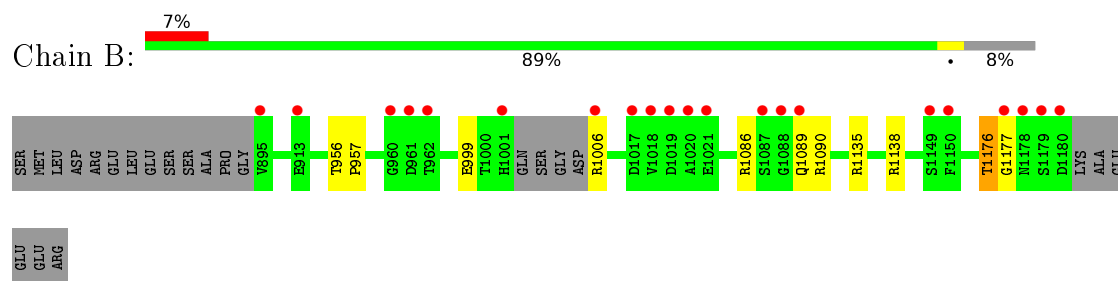
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Mycocerosic acid synthase-like polyketide synthase



- Molecule 1: Mycocerosic acid synthase-like polyketide synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.06Å 162.20Å 59.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.97 – 1.45 47.97 – 1.45	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.97-1.45) 99.3 (47.97-1.45)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.36 (at 1.45Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.149 , 0.177 0.149 , 0.178	Depositor DCC
$R_{free}$ test set	1997 reflections (1.74%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.0	Xtriage
Anisotropy	0.563	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 53.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	9282	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.61% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.54	0/2377	0.69	0/3246
1	B	0.50	0/2337	0.65	0/3191
All	All	0.52	0/4714	0.67	0/6437

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1000	THR	Peptide

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2234	2157	2134	5	0
1	B	2213	2121	2125	9	0
2	A	12	18	18	0	0
2	B	12	18	18	0	0
3	A	288	0	0	1	1
3	B	209	0	0	1	0
All	All	4968	4314	4295	14	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (14) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1162:ASP:O	3:A:1301:HOH:O	2.16	0.61
1:B:1006[B]:ARG:HB3	1:B:1006[B]:ARG:HH11	1.71	0.55
1:A:973:MET:O	1:A:1181:LYS:NZ	2.35	0.51
1:B:1176[B]:THR:HG22	1:B:1177:GLY:N	2.26	0.49
1:A:1115[B]:ILE:HG21	1:A:1148:ASP:O	2.14	0.47
1:B:1086[A]:ARG:NH2	1:B:1135:ARG:O	2.47	0.47
1:A:1181:LYS:HE3	1:A:1181:LYS:HB2	1.64	0.46
1:B:1090:ARG:O	3:B:1301:HOH:O	2.21	0.44
1:B:1086[A]:ARG:HH22	1:B:1138[A]:ARG:HH22	1.66	0.43
1:A:1038:ARG:NE	1:A:1064:GLU:OE2	2.40	0.42
1:B:999:GLU:OE2	1:B:1006[A]:ARG:HD2	2.20	0.41
1:B:956:THR:HB	1:B:957:PRO:HD3	2.03	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1488:HOH:O	3:A:1488:HOH:O[2_875]	2.14	0.06

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	310/305 (102%)	307 (99%)	3 (1%)	0	100	100
1	B	301/305 (99%)	293 (97%)	6 (2%)	2 (1%)	26	5
All	All	611/610 (100%)	600 (98%)	9 (2%)	2 (0%)	52	17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1176[A]	THR
1	B	1176[B]	THR

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	241/234 (103%)	239 (99%)	2 (1%)	86	66
1	B	236/234 (101%)	235 (100%)	1 (0%)	93	82
All	All	477/468 (102%)	474 (99%)	3 (1%)	92	73

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	970[A]	PHE
1	A	970[B]	PHE
1	B	1089	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	937	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	EDO	A	1201	-	3,3,3	0.45	0	2,2,2	0.63	0
2	EDO	A	1202	-	3,3,3	0.44	0	2,2,2	0.62	0
2	EDO	A	1203	-	3,3,3	0.38	0	2,2,2	0.43	0
2	EDO	B	1201	-	3,3,3	0.47	0	2,2,2	0.78	0
2	EDO	B	1202	-	3,3,3	0.44	0	2,2,2	0.69	0
2	EDO	B	1203	-	3,3,3	0.51	0	2,2,2	0.39	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	A	1201	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1202	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1203	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1201	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	B	1202	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1203	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	286/305 (93%)	0.23	16 (5%) 28 27	18, 27, 55, 71	0
1	B	282/305 (92%)	0.13	21 (7%) 17 18	20, 29, 56, 77	4 (1%)
All	All	568/610 (93%)	0.18	37 (6%) 22 22	18, 28, 56, 77	4 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1150	PHE	8.7
1	B	960	GLY	8.5
1	A	1182	ALA	6.0
1	A	1181	LYS	5.9
1	A	895	VAL	5.7
1	A	898[A]	VAL	5.2
1	B	1019	ASP	5.0
1	B	1178	ASN	5.0
1	B	895	VAL	4.5
1	A	1178	ASN	4.5
1	A	1019	ASP	4.5
1	A	1005	ASP	4.4
1	B	962	THR	4.4
1	A	1001	HIS	4.1
1	B	1021	GLU	3.8
1	B	1018	VAL	3.8
1	B	1177	GLY	3.6
1	B	961	ASP	3.4
1	A	1180	ASP	3.3
1	B	1017	ASP	3.2
1	B	1020	ALA	3.2
1	B	1089	GLN	3.1
1	A	962[A]	THR	2.9
1	B	1006[A]	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	1180	ASP	2.7
1	B	1179	SER	2.6
1	B	1088	GLY	2.5
1	B	1087	SER	2.4
1	B	913	GLU	2.4
1	A	960	GLY	2.4
1	A	991	PRO	2.2
1	A	1018	VAL	2.2
1	A	1116[A]	ALA	2.2
1	A	913	GLU	2.2
1	A	914	PRO	2.2
1	B	1001[A]	HIS	2.1
1	B	1149	SER	2.1

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	EDO	B	1203	4/4	0.97	0.10	3.67	38,46,47,47	0
2	EDO	A	1202	4/4	0.95	0.10	1.93	30,36,39,43	0
2	EDO	B	1202	4/4	0.83	0.12	1.83	51,61,63,66	0
2	EDO	A	1201	4/4	0.91	0.13	0.61	55,66,68,73	0
2	EDO	A	1203	4/4	0.94	0.08	0.21	41,51,60,62	0
2	EDO	B	1201	4/4	0.84	0.11	-0.10	49,58,59,60	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.